

FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'

ENTERED AT 15:13:18 ON 09 AUG 2006

L1 657493 S (INTERFERON OR IFN OR INF)
L2 24717 S L1(S) (VARIANT OR MODIFI? OR SUBSTITUT?)
L3 243 S L2(S) (HYDROPHOBIC OR (SOLVENT(W) EXPOSED))
L4 239 DUP REM L3 (4 DUPLICATES REMOVED)
L5 144 S L4 AND PY=<2003
L6 131 S L1(S) F8
L7 131 DUP REM L6 (0 DUPLICATES REMOVED)
L8 83 S L7 AND PY=<2003
L9 0 S AGUINALDO, ANNA/AU
L10 0 S BEYNA, AMELIA/AU
L11 0 S ANNA AGUINALDO/AU
L12 7 S DESJARLAIS, JOHN/AU
L13 84 S CHO, HO SUNG/AU
L14 14 S MARSHALL, SHANNON/AU
L15 22 S MUCHHAL, UMESH/AU
L16 3 S VILLEGAS, MICHAEL/AU
L17 15 S ZHUKOVSKY, EUGENE/AU
L18 17 S (L13 OR L14 OR L15 OR L15 OR L16 OR L17) AND L2

Refine Search

Search Results -

| Terms | Documents |
|-----------------------------------------------------------|-----------|
| (L6 or L7 or L8 or L9 or L10 or L11 or L13 or L14) and L2 | 19 |

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L15

Refine Search

Recall Text

Clear

Interrupt

Search History

DATE: Wednesday, August 09, 2006 [Printable Copy](#) [Create Case](#)

Set Name Query

side by side

Hit Count Set Name

result set

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR

| | | | |
|------------|-----------------------------------------------------------|------|------------|
| <u>L15</u> | (L6 or L7 or L8 or L9 or L10 or L11 or L13 or L14) and L2 | 19 | <u>L15</u> |
| <u>L14</u> | "Zhukovsky, Eugene"[IN] | 11 | <u>L14</u> |
| <u>L13</u> | "Villegas, Michael"[IN] | 4 | <u>L13</u> |
| <u>L12</u> | "Aquino, Michael"[IN] | 0 | <u>L12</u> |
| <u>L11</u> | "Muchhal, Umesh"[IN] | 16 | <u>L11</u> |
| <u>L10</u> | "Marshall, Shannon"[IN] | 24 | <u>L10</u> |
| <u>L9</u> | "Desjarlais, John"[IN] | 66 | <u>L9</u> |
| <u>L8</u> | "Cho, Ho Sung"[IN] | 15 | <u>L8</u> |
| <u>L7</u> | "Beyna, Amelia"[IN] | 4 | <u>L7</u> |
| <u>L6</u> | "Aguinaldo, Anna"[IN] | 6 | <u>L6</u> |
| <u>L5</u> | L1 with F8 | 16 | <u>L5</u> |
| <u>L4</u> | L2 same (hydrophobic or (solvent adj exposed)) | 52 | <u>L4</u> |
| <u>L3</u> | L2 with (hydrophobic or (solvent adj exposed)) | 30 | <u>L3</u> |
| <u>L2</u> | L1 with (variant or modifi\$7 or substitut\$4) | 6559 | <u>L2</u> |

L1 (interferon or IFN or INF)

86531 L1

END OF SEARCH HISTORY

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:13:12 ; Search time 198 Seconds
(without alignments)
383.323 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:22:12 ; Search time 51 Seconds
(without alignments)
284.904 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:22:52 ; Search time 178 Seconds
(without alignments)
431.987 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:23:52 ; Search time 29 Seconds
(without alignments)
327.467 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:17:07 ; Search time 39 Seconds
(without alignments)
409.538 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:13:42 ; Search time 298 Seconds
(without alignments)
515.277 Million cell updates/sec

Title: US-10-676-705-15
Perfect score: 874
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 11:59:17 ; Search time 195 Seconds
(without alignments)
389.220 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: July 15, 2006, 12:08:17 ; Search time 50 Seconds
(without alignments)
290.602 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: July 15, 2006, 12:08:57 ; Search time 186 Seconds
(without alignments)
413.407 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYL RN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:09:57 ; Search time 27 Seconds
(without alignments)
351.724 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:03:17 ; Search time 39 Seconds
(without alignments)
409.538 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

GenCore version 5.1.9
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QM protein - protein search, using sw model

Run on: July 15, 2006, 11:59:52 ; Search time 298 Seconds
(without alignments)
515.277 Million cell updates/sec

Title: US-10-676-705-15-GLU8
Perfect score: 873
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.